RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/648,692A_
Source: _IFW16_
Date Processed by STIC: _4/22/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
   Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos — was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering — use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
each n or Xaa can only represent a single residue. Please present the maximum number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug" — sequences(s) _____ . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.

7 ____ Skipped Sequences — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES) — (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES) — <210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's — Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) — Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response — scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
is Artificial Sequence

11 ____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug" — resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFW16

RAW SEQUENCE LISTING   DATE: 04/23/2004
PATENT APPLICATION: US/09/648,692A   TIME: 11:49:45

        Input Set : A:\Seqlist.txt
        Output Set: N:\CRF4\04232004\I648692A.raw

Does Not Comply
Correctod Diskette Needed

see item 4 on Error Summary Sheet

```
  4 <110> APPLICANT: Dolly, James Oliver
  5        Li, Yan
  6        Chan, C.K.
  7        Aoki, Kei Roger
  9 <120> TITLE OF INVENTION: Activatable Recombinant Neurotoxins
 12 <130> FILE REFERENCE: 17311(BO)
 14 <140> CURRENT APPLICATION NUMBER: 09/648,692A
 15 <141> CURRENT FILING DATE: 2000-08-25
 17 <150> PRIOR APPLICATION NUMBER: 60/150,710
 18 <151> PRIOR FILING DATE: 1999-08-25
 20 <160> NUMBER OF SEQ ID NOS: 29
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

ERRORED SEQUENCES

```
 91 <210> SEQ ID NO: 7
 92 <211> LENGTH: 65
 93 <212> TYPE: PRT
 94 <213> ORGANISM: Artificial Sequence
 96 <220> FEATURE:
 97 <223> OTHER INFORMATION: Engineered Intrachain loop region for C. tetani
 98        toxin
100 <400> SEQUENCE: 7
101 Ser Lys Leu Ile Gly Leu Cys Lys Lys Ile Ile Pro Pro Thr Asn Ile
102 1               5                   10                  15
103 Arg Glu Asn Leu Tyr Asn Arg Thr Ala Gly Glu Lys Leu Tyr Asp Asp
104             20                  25                  30
105 Asp Asp Lys Asp Arg Trp Gly Ser Ser Arg Ser Leu Thr Asp Leu Gly
E--> 106
    35              40              45          Gly Glu Leu Cys Ile
130 <210> SEQ ID NO: 10
131 <211> LENGTH: 4017
132 <212> TYPE: DNA
133 <213> ORGANISM: Clostridium botulinum
135 <400> SEQUENCE: 10
E--> 136 gaattcaagt agtagataat aaaaataatg ccacagattt ttattattaa taatgatata      60
137 tttatctcta actgtttaac tttaacttat aacaatgtaa atatatattt gtctataaaa     120
138 aatcaagatt acaattgggt tatatgtgat cttaatcatg atataccaaa aaagtcatat     180
139 ctatggatat taaaaaatat ataaatttaa aattaggaga tgctgtatat gccaaaaatt     240
140 aatagtttta attataatga tcctgttaat gatagaacaa ttttatatat taaaccaggc     300
141 ggttgtcaag aattttataa atcatttaat attatgaaaa atatttggat aattccagag     360
142 agaaatgtaa ttggtacaac cccccaagat tttcatccgc ctacttcatt aaaaaatgga     420
143 gatagtagtt attatgaccc taattatttt caaagtgatg aagaaaagga tagatttttta     480
```

```
144 aaaatagtca caaaaatatt taatagaata aataataatc tttcaggagg gatttttatta      540
145 gaagaactgt caaaagctaa tccatattta gggaatgata atactccaga taatcaattc      600
146 catattggtg atgcatcagc agttgagatt aaattctcaa atggtagcca agacatacta      660
147 ttacctaatg ttattataat gggagcagag cctgatttat ttgaaactaa cagttccaat      720
148 atttctctaa gaaataatta tatgccaagc aatcaccgtt ttggatcaat agctatagta      780
149 acattctcac ctgaatattc ttttagattt aatgataatt gtatgaatga atttattcaa      840
150 gatcctgctc ttacattaat gcatgaatta atacattcat tacatggact atatggggct      900
151 aaagggatta ctacaaagta tactataaca caaaaacaaa atcccctaat aacaaatata      960
152 agaggtacaa atattgaaga attcttaact tttggaggta ctgatttaaa cattattact     1020
153 agtgctcagt ccaatgatat ctatactaat cttctagctg attataaaaa aatagcgtct     1080
154 aaacttagca aagtacaagt atctaatcca ctacttaatc cttataaaga tgtttttgaa     1140
155 gcaaagtatg gattagataa agatgctagc ggaatttatt cggtaaatat aaacaaattt     1200
156 aatgatattt ttaaaaaatt atacagcttt acggaatttg atttacgaac taaatttcaa     1260
157 gttaaatgta ggcaaactta tattggacag tataaatact tcaaactttc aaacttgtta     1320
158 aatgattcta tttataatat atcagaaggc tataatataa ataatttaaa ggtaaatttt     1380
159 agaggacaga atgcaaattt aaatcctaga attattacac caattacagg tagaggacta     1440
160 gtaaaaaaaa tcattagatt ttgtaaaaat attgtttctg taaaaggcat aaggaaatca     1500
161 atatgtatcg aaataaataa tggtgagtta ttttttgtgg cttccgagaa tagttataat     1560
162 gatgataata taaatactcc taaagaaatt gacgatacag taacttcaaa taataattat     1620
163 gaaaatgatt tagatcaggt tatttttaaat tttaatagtg aatcagcacc tggactttca     1680
164 gatgaaaaat taaatttaac tatccaaaat gatgcttata taccaaaata tgattctaat     1740
165 ggaacaagtg atatagaaca acatgatgtt aatgaactta atgtattttt ctatttagat     1800
166 gcacagaaag tgcccgaagg tgaaaataat gtcaatctca cctcttcaat tgatacagca     1860
167 ttattagaac aacctaaaat atatacattt ttttcatcag aatttattaa taatgtcaat     1920
168 aaacctgtgc aagcagcatt atttgtaagc tggatacaac aagtgttagt agattttact     1980
169 actgaagcta accaaaaaag tactgttgat aaaaattgcag atatttctat agttgttcca     2040
170 tatataggtc ttgctttaaa tataggaaat gaagcacaaa aaggaaattt taaagatgca     2100
171 cttgaattat taggagcagg tatttttatta gaatttgaac ccgagctttt aattcctaca     2160
172 attttagtat tcacgataaa atctttttta ggttcatctg ataataaaaa taaagttatt     2220
173 aaagcaataa ataatgcatt gaaagaaaga gatgaaaaat ggaaagaagt atatagtttt     2280
174 atagtatcga attggatgac taaaattaat acacaattta ataaaagaaa agaacaaatg     2340
175 tatcaagctt tacaaaatca agtaaatgca attaaaacaa taatagaatc taagtataat     2400
176 agttatactt tagaggaaaa aaatgagctt acaaataaat atgatattaa gcaaatagaa     2460
177 aatgaactta atcaaaaggt ttctatagca atgaataata tagacaggtt cttaactgaa     2520
178 agttctatat cctatttaat gaaaataata aatgaagtaa aaattaataa attaagagaa     2580
179 tatgatgaga atgtcaaaac gtatttattg aattatatta tacaacatgg atcaatcttg     2640
180 ggagagagtc agcaagaact aaattctatg gtaactgata ccctaaataa tagtattcct     2700
181 tttaagcttt cttcttatac agatgataaa attttaattt catattttaa taaattcttt     2760
182 aagagaatta aaagtagttc agttttaaat atgagatata aaaatgataa atacgtagat     2820
183 acttcaggat atgattcaaa tataaatatt aatggagatg tatataaata tccaactaat     2880
184 aaaaatcaat ttggaatata taatgataaa cttagtgaag ttaatatatc tcaaaatgat     2940
185 tacattatat atgataataa atataaaaat tttagtatta gttttttgggt aagaattcct     3000
186 aactatgata ataagatagt aaatgttaat aatgaataca ctataataaa ttgtatgaga     3060
187 gataataatt caggatggaa agtatctctt aatcataatg aaataatttg gacattcgaa     3120
188 gataatcgag gaattaatca aaaattagca tttaactatg gtaacgcaaa tggtatttct     3180
189 gattatataa ataagtggat ttttgtaact ataactaatg atagattagg agattctaaa     3240
190 ctttatatta atggaaattt aatagatcaa aaatcaattt taaatttagg taatattcat     3300
191 gttagtgaca atatattatt taaaatagtt aattgtagtt atacaagata tattggtatt     3360
192 agatatttta atatttttga taaagaatta gatgaaacag aaattcaaac tttatatagc     3420
```

```
    193 aatgaaccta atacaaatat tttgaaggat ttttggggaa attatttgct ttatgacaaa    3480
    194 gaatactatt tattaaatgt gttaaaacca aataacttta ttgataggag aaaagattct    3540
    195 actttaagca ttaataatat aagaagcact attcttttag ctaatagatt atatagtgga    3600
    196 ataaaagtta aaatacaaag agttaataat agtagtacta acgataatct tgttagaaag    3660
    197 aatgatcagg tatatattaa ttttgtagcc agcaaaactc acttatttcc attatatgct    3720
    198 gatacagcta ccacaaataa agagaaaaca ataaaaatat catcatctgg caatagattt    3780
    199 aatcaagtag tagttatgaa ttcagtagga aattgtacaa tgaattttaa aaataataat    3840
E--> 200
ggaaataata ttgggttgtt aggtttcaag gcagatactg tcgttgctag tacttggtat    3900tatacacata
    243 <210> SEQ ID NO: 15
    244 <211> LENGTH: 5
    245 <212> TYPE: PRT
    246 <213> ORGANISM: Site  )invalid
    248 <220> FEATURE:          <213> response
    249 <221> NAME/KEY: SITE
    250 <222> LOCATION: (1)...(5)
    251 <223> OTHER INFORMATION: protease cleavage site
    253 <400> SEQUENCE: 15
E--> 254 Asp Asp Asp Asp Lys 1                    5
    271 <210> SEQ ID NO: 17
    272 <211> LENGTH: 5
    273 <212> TYPE: PRT
    274 <213> ORGANISM: Clostridium species
    276 <220> FEATURE:
    277 <221> NAME/KEY: ZN_FING
    278 <222> LOCATION: (1)...(5)
    279 <223> OTHER INFORMATION: Xaa=any amino acid
    281 <400> SEQUENCE: 17
E--> 282 His Glu Xaa Xaa His 1                    5
    295 <210> SEQ ID NO: 19
    296 <211> LENGTH: 22
    297 <212> TYPE: PRT
    298 <213> ORGANISM: Artificial Sequence
    300 <220> FEATURE:
    301 <223> OTHER INFORMATION: Linker
    303 <400> SEQUENCE: 19
E--> 304
Met Gly Gly Ser His His His His His His Gly Met Ala Ser Met Thr 1            5
    306 <210> SEQ ID NO: 20
    307 <211> LENGTH: 19
    308 <212> TYPE: PRT
    309 <213> ORGANISM: Clostridium botulinum
    311 <400> SEQUENCE: 20
E--> 312
Ser Leu Thr Asp Leu Gly Gly Glu Leu Cys Ile Lys Ile Lys Asn Glu 1           5
    325 <210> SEQ ID NO: 22
    326 <211> LENGTH: 7
    327 <212> TYPE: PRT
    328 <213> ORGANISM: Artificial Sequence
    330 <220> FEATURE:
    331 <221> NAME/KEY: SITE
    332 <222> LOCATION: (2)...(3)
```

(handwritten annotations:) see Item 4 on Error Summary Sheet; see item 10 on Error Summary Sheet (same error in sequence 16); item 4 (multiple)

```
      333 <223> OTHER INFORMATION: Xaa=any amino acid
      335 <223> OTHER INFORMATION: Protease cleavage site
W--> 337 <400> 22
E--> 338 Glu Xaa Xaa Tyr Ser Gln Ser 1                    5    idem 4
      340 <210> SEQ ID NO: 23
      341 <211> LENGTH: 7
      342 <212> TYPE: PRT
      343 <213> ORGANISM: Artificial Sequence
      345 <220> FEATURE:
      346 <221> NAME/KEY: SITE
      347 <222> LOCATION: (2)...(3)
      348 <223> OTHER INFORMATION: Xaa=any amino acid
      350 <221> NAME/KEY: SITE
      351 <222> LOCATION: (5)...(5)
      352 <223> OTHER INFORMATION: Xaa=any amino acid
      354 <223> OTHER INFORMATION: Protease cleavage site
W--> 356 <400> 23
E--> 357 Glu Xaa Xaa Tyr Xaa Gln Gly 1                5    idem 4
      359 <210> SEQ ID NO: 24
      360 <211> LENGTH: 18
      361 <212> TYPE: PRT
      362 <213> ORGANISM: Artificial Sequence
      364 <220> FEATURE:
      365 <223> OTHER INFORMATION: Translated PCR fragment        idem 4
      367 <400> SEQUENCE: 24
E--> 368
Met Arg Gly Ser His His His His His His Gly Ser Pro Lys Ile Asn 1          5
```

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\04232004\I648692A.raw

```
181 agttctatat cctatttaat gaaaataata aatgaagtaa aaattaataa attaagagaa    2580
182 tatgatgaga atgtcaaaac gtatttattg aattatatta tacaacatgg atcaatcttg    2640
183 ggagagagtc agcaagaact aaattctatg gtaactgata ccctaaataa tagtattcct    2700
184 tttaagcttt cttcttatac agatgataaa attttaattt catatttaa taaattcttt     2760
185 aagagaatta aaagtagttc agttttaaat atgagatata aaaatgataa atacgtagat    2820
186 acttcaggat atgattcaaa tataaatatt aatggagatg tatataaata tccaactaat    2880
187 aaaaatcaat ttggaatata taatgataaa cttagtgaag ttaatatatc tcaaaatgat    2940
188 tacattatat atgataataa atataaaaat tttagtatta gtttttgggt aagaattcct    3000
189 aactatgata ataagatagt aaatgttaat aatgaataca ctataataaa ttgtatgaga    3060
190 gataataatt caggatggaa agtatctctt aatcataatg aaataatttg gacattcgaa    3120
191 gataatcgag gaattaatca aaaattagca tttaactatg gtaacgcaaa tggtatttct    3180
192 gattatataa ataagtggat ttttgtaact ataactaatg atagattagg agattctaaa    3240
193 ctttatatta atggaaattt aatagatcaa aaatcaattt taaatttagg taatattcat    3300
194 gttagtgaca atatattatt taaaatagtt aattgtagtt atacaagata tattggtatt    3360
195 agatatttta atatttttga taaagaatta gatgaaacag aaattcaaac tttatatagc    3420
196 aatgaaccta atacaaatat tttgaaggat ttttggggaa attatttgct ttatgacaaa    3480
197 gaatactatt tattaaatgt gttaaaacca aataacttta ttgataggag aaaagattct    3540
198 actttaagca ttaataatat aagaagcact attcttttag ctaatagatt atatagtgga    3600
199 ataaaagtta aaatacaaag agttaataat agtagtacta acgataatct tgttagaaag    3660
200 aatgatcagg tatatattaa ttttgtagcc agcaaaactc acttatttcc attatatgct    3720
201 gatacagcta ccacaaataa agagaaaaca ataaaaatat catcatctgg caatagattt    3780
202 aatcaagtag tagttatgaa ttcagtagga aattgtacaa tgaattttaa aaataataat    3840
203 ggaaataata ttgggttgtt aggtttcaag gcagatactg tcgttgctag tacttggtat    3900
204 tatacacata tgagagatca tacaaacagc aatggatgtt tttggaactt tatttctgaa    3960
205 gaacatggat ggcaagaaaa ataaaaatta gattaaacgg ctaaagtcat aaattcc        4017
207 <210> SEQ ID NO: 11
208 <211> LENGTH: 37
209 <212> TYPE: DNA
210 <213> ORGANISM: Artifical Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: PCR primer
215 <400> SEQUENCE: 11
216 cccggatccc caaaaattaa tagttttaat tataatg                                37
218 <210> SEQ ID NO: 12
219 <211> LENGTH: 36
220 <212> TYPE: DNA
221 <213> ORGANISM: PCR primer
223 <400> SEQUENCE: 12
224 cccctgcagt catttttctt gccatccatg ttcttc                                 36
226 <210> SEQ ID NO: 13
227 <211> LENGTH: 31
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: PCR primer
234 <400> SEQUENCE: 13
235 cagttaatac attcattaca tggactatat g                                      31
237 <210> SEQ ID NO: 14
238 <211> LENGTH: 26
```

C--> (handwritten annotations: "Artificial" near line 208-210; "Artifical" circled at line 210; "PCR primer" circled with "invalid <213> response" at line 221)

Input Set : **A:\Seqlist.txt**
Output Set: **N:\CRF4\04232004\I648692A.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes
spaces.

Seq#:7; Line(s) 106
Seq#:10; Line(s) 200
Seq#:19; Line(s) 304
Seq#:20; Line(s) 312
Seq#:24; Line(s) 368

VERIFICATION SUMMARY   DATE: 04/23/2004
PATENT APPLICATION: **US/09/648,692A**   TIME: 11:49:46

Input Set : **A:\Seqlist.txt**
Output Set: **N:\CRF4\04232004\I648692A.raw**

```
L:106 M:252 E: No. of Seq. differs, <211> LENGTH:Input:65 Found:48 SEQ:7
L:200 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:10
L:200 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:200 M:252 E: No. of Seq. differs, <211> LENGTH:Input:4017 Found:3840 SEQ:10
L:205 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:254 M:301 E: (44) No Sequence Data was Shown, SEQ ID:15
L:254 M:252 E: No. of Seq. differs, <211> LENGTH:Input:5 Found:0 SEQ:15
L:282 M:301 E: (44) No Sequence Data was Shown, SEQ ID:17
L:282 M:252 E: No. of Seq. differs, <211> LENGTH:Input:5 Found:0 SEQ:17
L:304 M:301 E: (44) No Sequence Data was Shown, SEQ ID:19
L:304 M:252 E: No. of Seq. differs, <211> LENGTH:Input:22 Found:0 SEQ:19
L:312 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:337 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:338 M:301 E: (44) No Sequence Data was Shown, SEQ ID:22
L:338 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7 Found:0 SEQ:22
L:356 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:357 M:301 E: (44) No Sequence Data was Shown, SEQ ID:23
L:357 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7 Found:0 SEQ:23
L:368 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:430 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
```